

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 19:40:25 ; Search time 1774.61 Seconds  
(without alignments)  
5932.360 Million cell updates/sec

Title: US-09-597-771-11

Sequence: 1 aaagaatcctagagagagaa.....gcataaaaaaaaaaaaaa 780

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthu:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	707.4	90.7	736	10	BG126997 EST472643
2	695.2	89.1	761	10	BG128621 EST474267
3	660.4	84.7	692	10	BG129599 EST475245
4	632.4	81.1	703	10	BM111265 EST558801
5	632.4	81.1	708	10	BM408093 EST582420
6	630.8	80.9	708	10	BI179266 EST520211
7	617.8	79.2	708	10	BI433851 EST536599
8	617.4	79.2	646	9	BF113889 EST441479
9	616.4	79.0	646	9	AM621798 EST312596
10	613.8	78.7	637	9	AI491151 EST241860
11	612.2	78.5	654	9	AM622133 EST312930
12	603.8	77.7	624	10	BI203884 EST521924
13	603.2	77.3	622	10	BI205158 EST523198
14	588.4	75.4	617	10	BE451409 EST402297
15	579.8	74.3	645	10	BG590355 EST498197
16	578.4	74.2	636	10	BG131118 EST464010
17	573.4	73.5	694	10	BF460225 073A04 Ma

18	566.8	72.7	624	10	BG600393	BG600393 EST505288
19	560.4	71.8	599	9	AM649591	AM649591 EST328045
20	558	71.5	613	10	BG598608	BG598608 EST503508
21	557.6	71.5	600	9	AM650303	AM650303 EST328757
22	553.6	71.0	607	10	BI432185	BI432185 EST534946
23	541.4	69.4	552	9	AM039483	AM039483 EST281764
24	536.8	68.8	586	10	BG598846	BG598846 EST303746
25	535	68.6	635	10	BG598422	BG598422 EST497264
26	529.8	67.9	549	9	AM219868	AM219868 EST302351
27	529.4	67.9	549	9	AM621943	AM621943 EST312741
28	528.4	67.7	550	9	AI781299	AI781299 EST262178
29	522	66.9	549	10	BI208112	BI208112 EST526152
30	518.8	66.5	568	10	BM112206	BM112206 EST559742
31	518	66.4	583	10	BG890993	BG890993 EST16844
32	516.4	66.2	532	9	AI484872	AI484872 EST243133
33	516.2	66.2	544	9	AM649132	AM649132 EST327586
34	509.8	65.4	559	9	AM907082	AM907082 EST343114
35	505.8	64.8	555	10	BG098841	BG098841 EST463360
36	496.4	63.6	510	9	AM092208	AM092208 EST285304
37	492.8	63.2	518	9	AM625182	AM625182 EST319089
38	488.4	62.6	504	9	AI776147	AI776147 EST257235
39	482.4	61.8	506	9	AM094639	AM094639 EST287807
40	479.4	61.5	503	10	BF114414	BF114414 EST442004
41	479	61.4	493	10	BI209089	BI209089 EST527129
42	469.8	60.2	473	9	AM932090	AM932090 EST357933
43	461.4	59.2	477	9	AI898530	AI898530 EST267973
44	457.8	58.7	461	9	AM092305	AM092305 EST285485
45	457.4	58.6	475	10	BI434352	BI434352 EST537113

## ALIGNMENTS

RESULT 1  
BG126997 736 bp mRNA linear EST 31-JAN-2001  
LOCUS EST472643 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
DEFINITION cTOF14G7 5' sequence, mRNA sequence.  
ACCESSION BG126997  
VERSION BG126997.1 GI:12627185  
KEYWORDS EST.  
SOURCE  
ORGANISM  
tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
REFERENCE  
1 (bases 1 to 736)  
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,  
Hansen, C., Rønning, C. and Tanksley, S.  
Generation of ESTs from tomato shoot/meristem tissue  
Unpublished (2001)  
COMMENT  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.  
Location/Qualifiers

FEATURES  
source  
1..736  
/organism="Lycopersicon esculentum"  
/cultivar="7496"  
/db\_xref="taxon:4081"  
/clone="cTOF14G7"  
/clone\_id="tomato shoot/meristem"  
/tissue\_type="shoot/meristem"  
/dev\_stage="developing shoots from 4-6wks old plants"  
/lab\_host="SOLR"  
/note="Vector: pluscript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old 7496). Tissue  
was immediately frozen in liquid nitrogen."  
BASE COUNT  
221 a 136 c 165 g 214 t

Query Match 90.7%; Score 707.4; DB 10; Length 736;  
 Best Local Similarity 99.5%; Pred. No. 6.9e-126;  
 Matches 731; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

30 taagagagaagacgtgctgcgagagaacacacatttgaagtcgaagcagatgctgtgc 89  
 |||||  
 Db 2 TAGAGAGAGAGAGCTGTGCGAGCAGAGAACCTTTTGNACTCAAGGAGATCTGTG 61

90 ctcaaaacttccacagaagaagctggaaccatccgtaagaatggttacatcgtaacaa 149  
 |||||  
 Db 62 CTCAAAAACCTTCCACAGCAGAGCTGGAACCATCCGTAAGAAATGTTACCTTATCAA 121

150 aggcgcgtccctgcgaaggtgttgaaggtctccacttcaaaaactggaagaacaggaactgc 209  
 |||||  
 Db 122 AGGCGGTCCGCAAGGTTGTGAGGTCTCCACTTCAAAAACCTGGAAGCAGCAGCATGTC 181

210 taatgtcaacttctggaacatctgaacatctgaacatctgaacatctgaacatctgaac 269  
 |||||  
 Db 182 TAAATGTCACTTTGTGCAATGTGCAATTTCAATGGAAGAACTGGAAGATATCGTTCC 241

270 gtccctccacaactgtgtagtgcacatgttaacgcgaacgactatcagctgtagtat 329  
 |||||  
 Db 242 GTCCCTCCCAATTTGTATGTGCGACATGTTAACCCGATCCGATATCATGATGATAT 301

330 ctctgaagaatgttctgctcaacttctgaagaatgtgaagaacacagaatgacactcag 389  
 |||||  
 Db 302 CTCTGAAGATGTTTGTGCTCACTTTCTAGAAAGTGGAAGCAGAGATGACCTCAG 361

390 gcttccacacgaatgaacatctgctgaagaaggttaagaatggttccagaagaagaaga 449  
 |||||  
 Db 362 GCTCCCAACCGATGAATCTGTGAAGCAGGTTAAAGTGGTTCCAGAGGAAGAAAGGA 421

450 tcttctgtgtctgtttagtctgtagtgcagagagaagaatgaagccgttaagaatgt 509  
 |||||  
 Db 422 TCTTGTGTGTGTGTATGTGTGCGATGCGGAGAGAGAGATTTAACCCCTTTAAGATGT 481

510 tggtaaccaagaatgtagttagtcaatgagcgc -ataatcaatgcgaagaagcttaagaat 567  
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 Db 482 TGGTACCAAGATTTGTTATGTGATGCGAGCATATTAATCACTGCCAAGCTTTAAGCAT 541

568 tatcatcctaaatgtgtgaacttgaatacactagatataaactgtgttttttttttttt 627  
 |||||  
 Db 542 TATCATATCTTAATGTGTACTTGTATATCATATTAATTAATGTTTATTTGCACTG 601

628 ttcaaaacacagaagaagaacactgctgttagtgcagaagaatgtagtcttgaactt 687  
 |||||  
 Db 602 TTCAAAAACCAAGAAAGAAAGAACTGCTGTTATGCTAGAGAAAGTTTGGCTTGAAGCTT 661

688 tgacagcagatgtaactatgtaaaatctaac-ttttttttttttttttttttttttttt 746  
 |||||  
 Db 662 TGACAGCAAGTTGAACATATGGAATAATCTTCTTTTTTTGGTAAATAATCTGTC 721

747 tctgttaatgttttg 761  
 |||||  
 Db 722 TCGTTAATGTTTTC 736

RESULT 2  
 BGI28621 761 bp mRNA linear EST 31-JAN-2001  
 LOCUS BGI28621 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
 DEFINITION EST174267 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
 accession BGI28621  
 version BGI28621.1 GI:12628809  
 keywords EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Lycopersicon esculentum; Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; eusterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.

REFERENCE 1 (bases 1 to 761)  
 AUTHORS van der Hoeven, R., Bezzierides, J., Sun, H., Cho, J., Utterback, T.,  
 Hansen, C., Rønning, C. and Tanksley, S.  
 TITLE Generation of ESTs from tomato shoot/meristem tissue  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: CUCI  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES  
 source  
 1..761  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="CTOF21F13"  
 /clone\_1lb="tomato shoot/meristem"  
 /tissue\_type="shoot/meristem"  
 /dev\_stage="developing shoots from 4-6wks old plants"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Small expanding leaves from the growing tip were  
 taken from greenhouse plants (4-6wks old TA496). tissue  
 was immediately frozen in liquid nitrogen."

BASE COUNT 234 a 146 c 171 g 210 t  
 ORIGIN

Query Match 89.1%; Score 695.2; DB 10; Length 761;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-123;  
 Matches 731; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

1 aaagaatcctagaagaagaagaaggaatcctagaagaagaagatctcgagagaagaac 60  
 |||||  
 Db 23 AAGGAATCCTAGAGAGAGAGAGGAATCCTAGAGAGAGAGATGTGCGACCAAGAAC 82

61 catcttgagtcgaagcagaatgtgtgtgcctcaaaaacttccacagaagaatggaac 120  
 |||||  
 Db 83 CATTTGAGTCAGCAAGCAGATGCTGTGCTCAAAAATTTCCACAGCAAGCTGGAAC 142

121 atccgtaagaatggttacatcgtagtcaagaagccgtccctcgaaggttgaagcttc 180  
 |||||  
 Db 143 ATCCGTGAAGATGTTATCATCGTTATCAAGGCGCTCCGCAAGGTGTGAGGTCTC 202

181 acttcaaaaactggaagaacacagacatgttaaatgtcaacttctgcaacttgaacat 240  
 |||||  
 Db 203 ACTTCAAAAACCTGGAAGACACGAGCATGCTAAATGTCACCTTTGTGCAATTTG 262

241 aatgagaagaactggaagaatcgttcgtccctcccaaaatgtgagtgagcaatgtt 300  
 |||||  
 Db 263 AATGGAAGAAGAACTGGAAGATATGTTCCGTCCACAAATGTGATGTGCGACATGTT 322

301 aaccgtacgaactacagctgtagatatactctgaagaatggttcttcaactcttact 360  
 |||||  
 Db 323 AACCGTACCGACTATCAGCTGATTTGATATCTGGAAGATGTTTGTCTCACTTTACT 382

361 gaaagtgaagaacacagaagaatgagctccacagctgcaaaatcgtcgaagcag 420  
 |||||  
 Db 383 GAAAGTGGAAGACCAAGATGAGCTCAGGCTTCCACGATGAATAATCGTGAAGCAG 442

421 gtaagaatggttccagaagaagaagaatcctgtgtgtctgtttagtctgagatgggc 480  
 |||||  
 Db 443 GTTAAAGTGGGTTCCAGGAAGGAAGAAAGATCTGTGTGTATGTTGCGATGGGC 502

481 gaagacagatgaagccgttaa- ggtgtgtgtgacaaagaatgaatgtagtcatggcag 539  
 |||||  
 Db 503 GAAGACAGATTTAAGCGCGTTAAGGATGTTGTGTAACCAAGAAATTTAGTTATGTGACG 562

540 c-ataatcactgccaagctttaagacatataatcctaagtgtgtagtctgtagatc 597  
 |||||  
 Db 563 CATTTATCACTGCCAAAGCTTTAAGACATTAATATCCAAATGTGTGTTGATATC 622

598 actagatataaactgtgtattgtgcaactgttcaaaacagaagaagaagaatgctgtta 657

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Db 623 ACTAGATATTAACGTGTATTTCACCTGTTCAAAAGAAAGAAAGAAAGCTCTGTGA 682
QY 658 tggctagagaagaatttgcttgagcttgcagacagctgaactaigtgaattc 717
Db 683 TGGCTAGAGAAAGTATGCTTGTGAGCTTTT-ACAGCACAGTGAACATATGTGAAATTC 741
QY 718 tacttttttttttctg9 735
Db 742 TACTTTTTTTTTTTTTTGG 759

RESULT 3
Bg129599 692 bp mRNA linear EST 31-JAN-2001
LOCUS EST475245 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION ctop25E23 5' sequence, mRNA sequence.
ACCESSION Bg129599
VERSION Bg129599.1 GI:12629787
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 692)
AUTHORS Van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Konning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.

FEATURES
source
1..692
/organism="Lycopersicon esculentum"
/cultivar="T4A96"
/db_xref="taxon:4081"
/clone="ctop25E23"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old T4A96). Tissue
was immediately frozen in liquid nitrogen."

BASE COUNT 213 a 133 c 158 g 188 t

Query Match 84.7% Score 660.4; DB 10; Length 692;
Best Local Similarity 99.4%; Pred. No. 7e-117;
Matches 664; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 30 tagagagagaagcatgtcgagcagaagacacatttgagtcagaagcagatgtcgtgc 89
Db 2 TAGAGAGAGAGAGCATGTGCGAGCAGAGAACACCATTTTGAATGCAAGGAGATGCTGAGTC 61
QY 90 cttaaaaactttccacagcaagctggaacatctcgttaagatggttcatcgttatcaa 149
Db 62 CTAAAAAACTTTCCACACAGAGCTGGACCATCCGTAAGATGGTTACATCGTTATCAA 121
QY 150 aggcgcgtccctcgaagtggttgcagtcctcaactcaaaaactggaacacagacatgc 209
Db 122 AGGCCGTCCTGCAAGGTTGTGAGGTCCTCACTTCAAAAACCTGCAAGACGAGACATGC 181
QY 210 taatgtcactttgtggcaattgacatttcaatggaagaagaactggaagatatcgttcc 269
Db 182 TAAATGTCACTTGTGGCAATTGACATTTTCATATGGAAGAAACCTGGAAGATATCTGTTCC 241

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QY 270 gtcctccacaattgtgatgtgcacatgtaaccgtaaccgactatcagctgatatc 329
Db 242 GTTCCTCCACAAATTGTGATGTGCGACATGTTAACCGACATATACGTGATGTAT 301
QY 330 ctctgaagaatggtttgtctcaactcttactgaagaatggaacacagaatgacctcag 389
Db 302 CTTGAGAGATGGTTTGTCTCAGCTTTACTTACGAAAGTGGAACACCAAGATGACCTCAG 361
QY 390 gtttccacagatgaaaatctgctggaagcaggttaagaatggttccagaagaagaaga 449
Db 362 GCTTCCACCGATGAATAATCTGCTGAAGCAGATTAAAGATGGTTCCAGGAAGGAAGA 421
QY 450 tcttgcgtgtctgtatgctgcagatggcggaagacagatlaacgcgtlaagagatg 509
Db 422 TCTTGGGAGTGTTTATGCTGCGATGGCGAAGACAGATTAAACCCCTTAAGCATGT 481
QY 510 tggatccagaatttgatgtatgtcatgtgcagc-ataatcctgcgaagcttaagcatt 567
Db 482 TGTACCAAGAAATTGATTATGTCATGCGACATTAATCACTGSCAAAGCTTTAAGCAT 541
QY 568 tatcatcctaatgttggttacttgatatacactagattataaactggttattgcactg 627
Db 542 TATCATATCTTAATGTGGTACTTGTATATCACTGATTAATTAAGTATTATTCACATG 601
QY 628 ttcaaaacaaaagaagaagaactgctgttatgctgtagaagaagaatggttgaagctt 687
Db 602 TTCAAAACAAAAGAAAGAAAGAACTGCTGTATGGCTAGAGAAAGTATGGCTTGAAGCTTT 661
QY 688 tgacagcagatgtgaactatgaaat 715
Db 662 TG-CAGCACAGTTGAACATATGTGAATAAT 688

RESULT 4
Bm111265 703 bp mRNA linear EST 26-NOV-2001
LOCUS EST558801 potato roots Solanum tuberosum cDNA clone cPHO1F18 5'
DEFINITION end, mRNA sequence.
ACCESSION Bm111265
VERSION Bm111265.1 GI:17073666
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 703)
AUTHORS Van der Hoeven,R., Sun,H., Karanycheva,S.A., Tsai,J., Van Aken,S.,
Utterback,T., Chleming,A., Bougri,O., Buell,C.R., Konning,C.,
Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
JOURNAL Unpublished (2001)
COMMENT Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: Please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.

FEATURES
source
1..703
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPHO1F18"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium."

```

Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

BASE COUNT 218 a 143 c 158 g 184 t

ORIGIN

Query Match 81.1%; Score 632.4; DB 10; Length 703;  
Best Local Similarity 95.9%; Pred. No. 1.6e-111;  
Matches 660; Conservative 0; Mismatches 26; Indels 2; Gaps 1;

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Oy 20 aaggaatcctagagagaagcaatgctgcgaagaaacacattttagatcaaaagcag 79
Db 1 AAGGGAATCCTAGAGAGAAGCAAGCATGTGGAAGCAACACCATTTTGAACAAAGCGC 60
Oy 80 atgctggtgctcctcaaaacttcccaagcaagctggaacatccgttaagaatgttaca 139
Db 61 ATGCTGTCCTCAAAAACCTTACCACAGCAAGCTGGAACCATCCGTAAAGATGTTACA 120
Oy 140 tggatataaagacgctccctcgaagttgttgaagttcccaattcaaaaactggaagc 199
Db 121 TCGTATCAAAAGCCGCTCCCTCCAGAGTTGTTGAGGTCTCCACTTCAAAAACGTGAAGC 180
Oy 200 acggaacatgctaactgctcattgtgcgaattgacatttcaatggaagaagaactggaag 259
Db 181 ACGGACATGCTAAATGCTACTTGTGGCAATTGACATTTTCAATGGAAGAAGAACTCGAAG 240
Oy 260 atatgctccgctcccccgaattgtgatgtgcacatgtaacgcttcggaactacagc 319
Db 241 ATATTCGTTCCATCCCTCCCAATGTGAGCTGCCACATGTCACCGTCACGCTATACGC 300
Oy 320 tgaatgatactcctgaagaatgttctgctcaactcttaactgaagtgaaacccaag 379
Db 301 TGATTACATCTCTGAAGATGGTTTGTCTCCCTTCTTACTGAAGTGGAAACACCAAGG 360
Oy 380 atgacctcaggtctccaccgaatgaaatctgctgaagcaggctaaagaatggtccag 439
Db 361 ATGACCTCGGCTTCCACCGATGAAGTCTGCTGAAGCAGGTAAAGTGGTTCAGG 420
Oy 440 aaggaagaagatctgtgtgtctgtatgtctgcgaatggcggaagaagcagatcaacgc 499
Db 421 AAGGAAAGGATCTTGTGGTGTCTGTATGTCTGCGATGGGCCAAGACGATTAATGCCA 480
Oy 500 ttaaggaatgtgttaccagaatlaatgtaatgacatgacagcat--aatcactgcgaagc 557
Db 481 TTAAAGATATGTGTACCAAGAAATTAGTGTGCGCGACATCATTAATCATGCAAAAGC 540
Oy 558 ttaagaacatlatcatcctaagtgtgtaacttgatatacactagatataaacgtgtt 617
Db 541 TATTAAGACATCATTAATATCTTAATGTGGTACTTTGATATCAGATTAATAACTCTGT 600
Oy 618 atttcacgtcttcaaaaagaagaagaagaactgctgttatagtgctagaagaatgtgc 677
Db 601 ATTTCGCTTTGAAAACAAAAGAAAACGCTGCTATGCTTGAGAAAGTATTTGSC 660
Oy 678 tttagacttttgacagcagatgtaact 705
Db 661 TTGAGCTTTTGACAGCAGCTGAAGT 688
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RESULT 5  
LOCUS BM408093 708 bp mRNA linear EST 22-JAN-2002  
DEFINITION EST582420 potato roots Solanum tuberosum cDNA clone cPRO3307 5' end  
ACCESSION BM408093  
VERSION BM408093.1 GI:18259723  
KEYWORDS EST.  
SOURCE Solanum tuberosum  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; eunasterids I; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 708)

AUTHORS van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,  
Utterback,T., Chleminigo,A., Bougri,O., Buell,C.R., Romning,C.,  
Tanksley,S. and Baker,B.  
Generation of ESTs from potato roots  
Unpublished (2001)  
CONTACT: Research Genetics, Libraries Division  
Tel: 1-800-711-6195  
Email: cdna@resgen.com  
For clone info: please contact Research Genetics, Libraries  
Division tel.1-800-711-6195, email cdna@resgen.com  
Seq primer: T3

FEATURES  
source Location/Qualifiers  
1..708  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cPRO3307"  
/clone\_lib="potato roots"  
/tissue\_type="roots"  
/dev\_stage="in vitro grown stem cuttings"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Cornell University, Tanksley lab;  
sequencing: The Institute for Genomic Research. Roots were  
isolated from in vitro grown stem cuttings on CM medium.  
Roots were isolated two weeks after placing the stem  
cuttings from in vitro grown plants on medium."

BASE COUNT 219 a 142 c 158 g 189 t

ORIGIN

Query Match 81.1%; Score 632.4; DB 10; Length 708;  
Best Local Similarity 95.9%; Pred. No. 1.6e-111;  
Matches 660; Conservative 0; Mismatches 26; Indels 2; Gaps 1;

```
Oy 20 aaggaatcctagagagaagcaatgctgcgaagaaacacattttagatcaaaagcag 79
Db 1 AAGGGAATCCTAGAGAGAAGCAAGCATGTGGAAGCAACACCATTTTGAATCAAAAGCGC 60
Oy 80 atgctggtgctcctcaaaacttcccaagcaagctggaacatccgttaagaatgttaca 139
Db 61 ATGCTGTCCTCAAAAACCTTACCACAGCAAGCTGGAACCATCCGTAAAGATGTTACA 120
Oy 140 tggatataaagacgctccctcgaagttgtgtgagttctcacttcaaaaactggaagc 199
Db 121 TCGTATCAAAAGCCGCTCCCGAAGGTGTTGAGGTCTCCACTTCAAAAACGTGAAGC 180
Oy 200 acggaacatgctaactgtcacttgtgcgaattgacatttcaatggaagaagaactggaag 259
Db 181 ACGGACATGCTAAATGTCTTTGTGGCAATTGACATTTTCAATGGAAGAAGAACTCGAAG 240
Oy 260 atatgctcgtctccccaactgtgaatgtgcacatgtaacatgtaacgtaacgactacaag 319
Db 241 ATATGCTTCATCCCTCCCAATGTGACGTGCACATGTCAACCGATCAATATAGC 300
Oy 320 tgaatgatactcgaagaatgttttgtctcactcttaactggaagtggaaacccaag 379
Db 301 TGATTGACATCTGTAAGATGTTGTGTGCTCCCTTCTTACTGAAGTGAAGCAACCAAG 360
Oy 380 atgacctcaggtctcccaagcaagaatctgctgaagcaggttaagaatggttccaag 439
Db 361 ATGACCTCGGCTTCCACCGATGAAGTGTGCAACAGCAAGTAAAGATGGTTCCAGG 420
Oy 440 aaggaagaatctgtgtgtctgtatgtctgcgaatggcggaagaagaatgtaagcgc 499
Db 421 AAGGAAGATCTTGTGTGTCTGTTATGCTGCGCATGGGGAAGAGCAGATTAATGCCA 480
Oy 500 ttaagaatgtgtacaaagaatlaatgtaatgacatgacagcat--aatcactgcgaagc 557
Db 481 TTAAAGATATGTGTCAAGAAATTGATTATGCGGGGAGATCATTAATCATGCAAAAGC 540
Oy 558 ttaagaacatlatcatcctaagtgtgtaacttgatatacactagatataaactgtgtc 617
Db 541 TATTAAGACATCATTAATATCTTAATGTGGTACTTTGATATCAGATTAATAACTCTGT 600
```

Db 541 TATAAGACATTATATATCTATATGTAATTGTAATCATCTAGATACATCTCTGT 600

QY 618 attgcactgttcaaaaacaaagaactgctgtatggttagagagaattggc 677  
|||||  
Db 601 ATTGGACGTGTTGAAAACAAAAGAAAACGTGCTGTAGAGTAAGATGTGC 660  
|||||

QY 678 tttagcttttgacagcacagtgaact 705  
|||||  
Db 661 TTTGACCTTTTGACAGCACAGTTGAAGT 688  
|||||

RESULT 6  
BI179266 708 bp mRNA linear EST 09-JUL-2001  
LOCUS BI179266  
DEFINITION EST520211 CSTE Solanum tuberosum cdna clone cste1/P20 5' sequence,  
mRNA sequence.  
ACCESSION BI179266 GI:14645077  
VERSION BI179266  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 708)  
van der Hoeven, A., Bezzerides, J., Bachem, C., Vissers, R., Cho, J.,  
Chiemingo, A., Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and  
Baker, B.  
Generation of ESTs from in vitro grown microtubers  
Unpublished (2001)  
JOURNAL Contact: Cathy Ronning  
COMMENT The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.

FEATURES  
source location/Qualifiers  
1..708  
/organism="Solanum tuberosum"  
/cultivar="Bintje"  
/db\_xref="taxon:4113"  
/clone="cste1/P20"  
/clone\_lib="CSTE"  
/tissue\_type="axillary buds of stem explants; growing  
sink-tubers"  
/dev\_stage="7, 8 and 10 days"  
/lab\_host="SOLR"  
/note="vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; tissue supplied by Christian Bachem and Richard  
Vissers (Department of Plant Breeding, Wageningen  
University, The Netherlands). The csta libraries will  
attempt to capture the induction and initiation/initial  
growth of the tuber in an in vitro system as described in  
Bachem et al. (Plant Journal, 1996). Small microtubers  
develop from axillary buds attached to stem explants when  
placed on a high sucrose medium (10%). Visible  
morphological changes occur synchronously at day five in  
the axillary buds. The first library, csta (1-20) consists  
of axillary buds harvested on days 1-3. This targets  
those genes involved in induction of the microtubers. The  
following libraries, csta (21-40) and csta (41-60),  
capture genes involved in tuber initiation and outgrowth.  
This library is noted as p3 in Tanksley lab notebooks."

BASE COUNT 220 a 142 c 157 g 189 t

ORIGIN

Query Match 80.9%; Score 630.8; DB 10; Length 708;  
Best Local Similarity 95.8%; Pred. No. 3.2e-111;  
Matches 659; Conservative 0; Mismatches 27; Indels 2; Gaps 1;

QY 20 aaggaatccctagagagagcatgtgcgcgaagaacaccattttagtccaagcgag 79  
|||||  
Db 1 AAGGAAATCTTAGAGAGATGTCGACGAAGACACCACTTTGAGTCAAAAGCGAG 60  
|||||

QY 80 atgctgctcctcaaaaacttccacagcaagctggaaaccatccgtaagaatgttaca 139  
|||||  
Db 61 ATGCTGAGCTCCAAAACCTTACCACAGCAAGCTGGAAACATCCGTAAGAAATGTTACA 120  
|||||

QY 140 tcgtatcaaaagcgccgtccctgcgaaggtgtgttaggtctccacttcaaaaactygaaac 199  
|||||  
Db 121 TCGTTATCAAAAGCGCGTCCCGCAAGGTTGAGGCTCCACTTCAAAAACCTGGAAGC 180  
|||||

QY 200 aaggaatcgtcaaatgtcactttgtgcaattgtacatttcaatggaaagaacttgaag 259  
|||||  
Db 181 ACGGACATGCTAAATGTCTCTTTGTGGCAATTTGCAATTTGAAAGAAATCTCGAAG 240  
|||||

QY 260 atatgctcgcctccaccacaattgtatgtgcacatgttaaccgttaccgactatcagc 319  
|||||  
Db 241 ATATGCTGCATCTCCACCAATTTGTGACGTCACATGTCAACGTAAGTACTATCAGC 300  
|||||

QY 320 tgattgatatctcgtgaagatgttttgttctacttcttacttgaagtggaaacccaag 379  
|||||  
Db 301 TGATTGACATCTGTGAAGATGTTTGTCTCCCTTACTGAAAAGTGGAACACCAAGG 360  
|||||

QY 380 atgacctgaagcttccaccagatgaaaactcgtcgaagcaggttaagaatgggttcag 439  
|||||  
Db 361 ATGACCTCGGCTTCCACCGATGAAGTGTGTCGAAGCAAGTTAAAGATGGTTCAGG 420  
|||||

QY 440 aaggaagaagatcctgtgtgtctgtctgtatgtctgcgatggcggaagcagaattaagcg 499  
|||||  
Db 421 AAGGAAGAAGATCTGTGTGTGTCTGTATGTCTGATGGGGAAGACACATTAATGCCA 480  
|||||

QY 500 ttaagagatgtgtaccagaagattgattgtacatgcagcat--aatcactcccaagc 557  
|||||  
Db 481 TTAAGATATTTGGTACCAAGAAATTAGTTGTCCCGGACATCATTAATTCCTGCCAAGC 540  
|||||

QY 558 ttaagaatatacatatccctaattgtgtactttgatactagatataaactgtgt 617  
|||||  
Db 541 TATAAGACATCATATATATCTTAATGTGTAATTGATATCATCATGATTAATTAACCTGTT 600  
|||||

QY 618 attgcactgttcaaaaacaaagaactgctgtatggttagagagaattggc 677  
|||||  
Db 601 ATTGGACGTGTTGAAAACAAAAGAAAACGTGCTGTAGAGTAAGATGTGC 660  
|||||

QY 678 tttagcttttgacagcacagtgaact 705  
|||||  
Db 661 TTTGACCTTTTGACAGCACAGTTGAAGT 688  
|||||

RESULT 7  
BI433851 708 bp mRNA linear EST 21-AUG-2001  
LOCUS BI433851  
DEFINITION EST536599 P. Infestans-challenged leaf Solanum tuberosum cdna clone  
PCR8J11 5' sequence, mRNA sequence.  
ACCESSION BI433851 GI:15258528  
VERSION BI433851  
KEYWORDS EST.  
SOURCE potato.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 708)  
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemingo, A.,  
Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.  
Generation of ESTs from Potato Leaves Challenged with Phytophthora  
Infestans, Compatible Interaction  
Unpublished (2000)  
JOURNAL Contact: Cathy Ronning  
COMMENT The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.

FEATURES  
source location/Qualifiers  
1..708  
/organism="Solanum tuberosum"

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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="PCB311"
/clone_lib="P. infestans-challenged leaf"
/tissue_type="Leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Whole plants were challenged with 450,000
sporangia/ml P. infestans US-1(US 940501) in Blottron
(Madison, Wisconsin). Leaf tissue was collected at 1, 2,
5, 12, and 24 hours post-challenge and frozen in liquid
nitrogen immediately upon removal. Kennebec plants showed
no signs of HR. Kathadin plants (susceptible to P.
infestans US-1) were used as controls and showed
infection. NOTE: We cannot exclude the possibility that
this sequence is actually derived from Phytophthora rather
than potato."

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BASE COUNT      218 a      143 c      160 g      187 t
ORIGIN
Query Match      79.2%; Score 617.8; DB 10; Length 708;
Best Local Similarity 94.5%; Pred. No. 9.9e-109;
Matches 674; Conservative 0; Mismatches 32; Indels 7; Gaps 3;

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QY 20 aaggaatcctagaagaagaacatgctggacgaagaacacatttgaagaaagcag 79
DB 1 AAGGAAATCTTAGAGAGAGAGAGATGCGAGAGAGACCAATTTTGAAGTAAAGCGCAG 60
QY 80 atgctggtcctcaaaaactttccacagaagctggaacacatccgtaagaattggttaca 139
DB 61 ATGCTGGTGGCTCAAAAACATTACCCACAGCAAGCTGGAACCATCGTAGAATGAGTTACA 120
QY 140 tegtatacaaaagcgtccctcgaagtggtggaagctccatccatcaaaactgtgaaac 199
DB 121 TCGTTATCAAAAGCCCTCCCTCGCAAGTTGTGAGGCTCTCCACTTCAAAAACCTGGAAAC 180
QY 200 acgagacgtgaatgctccttctgtgcaattgacatttcaatggaagaacacggaag 259
DB 181 ACGGACATGCTAAATGCTCACTTGTGCAATGACATTTTCAATGGAAGAATCGGAAG 240
QY 260 atatcgttcctcccccacaatgtgattgtgacacatgttlaacgctacgaactatcagc 319
DB 241 ATATCGTTCATCTCCCAATATTGACGTGCAATGTCACACCTACCGCATATCAAC 300
QY 320 tgaatgatactctgaagatggttctgtctccttcttcaatgaatggaagaacacgaag 379
DB 301 TGAATGACATCTCTGAAGATGGTTGTCTCCTTCTTACTGAAAGTGAACACCAAGG 360
QY 380 atgacctcaggtctccacacgaatgaataatctgtgaagcaggttlaaagaatgggttcag 439
DB 361 ATGACCTCGCGCTTCCACCGATGAAGTCTGCTGAAGCAGGTTAAAGATGGGTCCAGG 420
QY 440 aaggaagaagatcttctgtgtctgtatgtctggaatggtgcaagacgaatgaacgag 499
DB 421 AAGGAAGAAGATCTTGTGTGTCTGTATGTCTGCGATGGCGCAAGAGCAGATTAAGCCA 480
QY 500 ttaagaatgtgttaccagaatattgattgcatatgacagcat--aataacgccaagc 557
DB 481 TTAAGGATATTGGTACCAAGATTAATGATGCGCGGCAATCAATAATACGCCAAAC 540
QY 558 ttaagaacatcatatacctaattgtgtaacttgaatacactagaatlaaactgtgtt 617
DB 541 TATAAGACATTATTATATCTTAATGTGTACTTTGATATCAGTAGATTCACCTCTCTGCT 600
QY 618 attgacacttcaaaaacaaagaagaacgctggttaagctgagaaagtattgac 677
DB 601 ATTGGCACTGTTGAACAAAGAAAG-AAAATGCTGCTATGAGCTTAGAAGAAATATTGGC 659
QY 678 ttggaagcttgcagacacagtgtaactatgtgaaatcttaactttttttt 730
DB 660 TTTGAGCTTTTGAACAGACAGTTGA---GTGGAATCTCTACTTTTAAATTAT 708

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RESULT      8
LOCUS      BF113889      646 bp      mRNA      linear      EST 18-May-2001
DEFINITION EST441479 tomato root, plant at pre-anthesis Lycopersicon
ACCESSION   BF113889
VERSION     BF113889
KEYWORDS    EST.
SOURCE      BF113889.1 GI:10943579
ORGANISM    tomato.
            Lycopersicon esculentum
            Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
            1 (bases 1 to 646)
REFERENCE   1
AUTHORS    van der Hoeven,R.S., Kochian,L., Garvin,D., Matern,A.L., Holt,I.E.,
            Liang,F., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W.,
            Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
            Generation of ESTs from tomato root tissue, pre-anthesis stage
            Unpublished (2000)
COMMENT     Contact: CUCI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES
            source
            1..646
            /organism="Lycopersicon esculentum"
            /cultivar="TA496"
            /db_xref="taxon:4081"
            /clone="CLEY23E19"
            /clone_lib="tomato root, plant at pre-anthesis"
            /tissue_type="root"
            /dev_stage="pre-anthesis stage"
            /note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
            XhoI; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY
            14850)."

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BASE COUNT      200 a      130 c      147 g      169 t
ORIGIN
Query Match      79.2%; Score 617.4; DB 10; Length 646;
Best Local Similarity 99.5%; Pred. No. 1.2e-108;
Matches 630; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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```

QY 1 aagaatcctagaagaagaagaatcctcctagaagaagaacatgctggacgaagaacac 60
DB 14 AAGGATCTTAGAGAGAGAGAGATCTTAGAGAGAGAGATGCGAGAGAGAGAGAGAGAG 73
QY 61 catltgagtaaaagcagatgctgtgctcctcaaaaacttccacagaagctggaac 120
DB 74 CATTTGAGTCAAAAGCGAGATGCTGTGCTCAAAAACCTTCCACAGCAAGCTGGAAC 133
QY 121 atcgtgaagaatggttatacgttataaagcgcgtccctcgaagtggttgaagctcc 180
DB 134 ATCCGTAAAGATGTTATCATCTTATCAAAAGCCGCTCCCTGCAAGTTGTGAGGTTCC 193
QY 181 acttcaaaaacttggaacacggaacatgctaaatgtaacttctgtggaatgacatttc 240
DB 194 ACTTCAAAAACCTGGAACACAGGACATGCTAAATGTCATCTTGTGGCAATTGACATTTTC 253
QY 241 aatggaagaacactggaagatatacgttccgtccctcccaaatgtgatatgacatgtt 300
DB 254 AATGGAAGAAGAACTGGAAGATATGTTCCGTCCTCCCAATTTGTGATGTGCCACAGTT 313
QY 301 aacgttaccgactatcagctatgatatatctcgaagaatggttctgtcactcttact 360
DB 314 AACCGTACCGACTATCACCTGATATGATATCTGTGAAGATGGTTTGTCTCACTTTACT 373
QY 361 gaaagtgaacaacaaagatgacctcaggttccacagatgaanaatctgtgaaagcag 420

```

Db 374 GAAAGTGAAGACCAAGGATGACCTGCTCCACCGATGAATAATCTGCTAGAGAC 433

QY 421 gttaaagatgggtccaggaaagaaagatcttgggtgtctgtatcttgcagatggc 480

Db 434 GTTAAAGATGGGTCCAGGAAGAAAGATCTGTGTCTGTATGTCTGCAGATGGC 493

QY 481 gaagacacattaaagccgttaagatgttggtaacaaagaattagttatgtcatatggcgc 540

Db 494 GAAAGACATTTACGCCCTTTAAGCATGTGGTACCAAGAAATTTATGTCAATGGCAGC 553

QY 541 --ataactcgtccaagcttaagacattacatactcaatgtgtactttgatca 598

Db 554 ATATATCACTGCGAAAGCTTAAAGCATATCATATCTCATATGTGTACTTTGATATCA 613

QY 599 ctagattataaactgtgtattgttgcactgttca 631

Db 614 CTAGATTATAAAGCTGTATTATTGCACTGTTC 646

RESULT 9

AM621798 646 bp mRNA linear EST 18-MAY-2001

LOCUS

DEFINITION EST132596 tomato root during/after fruit set, Cornell University

ACCESSION Lycopersicon esculentum cDNA clone CLEX13114.5, mRNA sequence.

VERSION AM621798

KEYWORDS AM621798.1 GI:7333445

SOURCE EST.

ORGANISM tomato.

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 646)

van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Kochian,L., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Romling,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

REFERENCE

AUTHORS

Generation of ESTs from tomato root, during and after fruit set

Unpublished (1999)

TITLE

JOURNAL

CONTACT: CUGI

COMMENT

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

FEATURES

location/Qualifiers

1..646

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CLEX13114"

/clone\_lib="tomato root during/after fruit set, Cornell University"

/tissue\_type="root"

/dev\_stage="plants during and after fruit set"

/note="Vector: pBluescript SK(-); Site1: EcorI; Site2: XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."

BASE COUNT

199 a 130 c 148 g 169 t

ORIGIN

Query Match 79.0%; Score 616.4; DB 9; Length 646;

Best Local Similarity 99.5%; Pred. No. 1.9e-108;

Matches 629; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 aagaatcttagagagaagaagatccttagagagaagaatgtcgagcaagaagacac 60

Db 15 AAGAAATCTCTAGAGAGAGAAAGGAATCTTAGAGAGAGAGCATGTGCGACGAAGAACAC 74

QY 61 cattttagtcacaagcagatgtgtgtcctcaaaacttccacagcaagctgaacc 120

Db 75 CATTTTAGTCMAAGGACAGATGCTGTGCTCTCAAAAACTTCCACAGCAAGCTGGAAC 134

QY 121 atccgtagaatggttacatcgttatacaaaagccgtccctgcgaaggtgtgtgaattcc 180

Db 135 ATCCGTAAGATGGTTCATCGTTATATCAAAAGGCCGCTCCGCAAGGTTGTTGAGGTCTCC 194

QY 181 acttcaaaacttgnaaaacacgcagatgtaaatgtactttgtggaatgtgacatttc 240

Db 195 ACTTCAAAAACCTGGAAGACGACGACATGCTAAATGTCACTTTGTGGCAATTTGACATTTTC 254

QY 241 aatgaaagaagaactcggaagatctcgtccgtccctcccaaatgtgtatgccaacatgtt 300

Db 255 AATGAAAGAAACATGGAAGATATGTTCCGTCCTCCACAAATGTGATGTGCCACATGTT 314

QY 301 aaccgtaccgactatcagctgtatgtatctctgaagaatgtgttctcacttact 360

Db 315 AACCGTACCGCTATCAAGCTGATGATATCTGMAAGATGTTTGTCTCACTTCTACT 374

QY 361 gaagttgaaacaccacagatgacatcagcttcacacacgcatgaataatctgctgaagcag 420

Db 375 GAAAGTGAAGAACCAAGAGATGACCTCAAGCTTCCACCATGAATAATCTGTGAAGACAG 434

QY 421 gttaaagatgggtccaggaaagaaagatcttgggtgtctgttlatgtctgcagatggc 480

Db 435 GTTAAAGATGGGTCCAGGAAGAAAGATCTGTGTGTCTGTATGTCTGCGATGGC 494

QY 481 gaagacagattaacgcccgttaagatgttggtaacaaagaattagttatgtcatggcgc 540

Db 495 GAAAGACAGATTAAGCGCCGTTAAAGATGTTGTACCAAGAAATTAATGTATGTCAATGGCAGC 554

QY 541 --ataactcgtccaagcttaagacattacatactcaatgtgtactttgatca 598

Db 555 ATATATCACTGCGAAAGCTTAAAGCATATCATATCTCATATGTGTACTTTGATATCA 614

QY 599 ctagattataaactgtgtattgttgcactgttc 630

Db 615 CTAGATTATAAAGCTGTATTATTGCACTGTTC 646

RESULT 10

AT491151

LOCUS

DEFINITION EST241860 tomato shoot, Cornell Lycopersicon esculentum cDNA clone CLEB3K4, mRNA sequence.

ACCESSION AT491151

VERSION AT491151.1 GI:4386461

KEYWORDS EST.

SOURCE

tomato.

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 637)

van der Hoeven,R.S., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Romling,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.

REFERENCE

AUTHORS

Generation of ESTs from tomato shoot meristem

Unpublished (1999)

TITLE

JOURNAL

CONTACT: CUGI

COMMENT

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

location/Qualifiers

1..637

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CLEB3K4"

/clone\_lib="tomato shoot, Cornell"

/tissue\_type="shoot meristem"



```

/dev.stage="8 week old plants"
/lab.host="X10LR"
/note="Vector: PK.CMV, Site_1: EcoRI, Site_2: XhoI, CLEB
-tomato Shoot Meristem EST Library. Oligo-dT primed cDNA
library made from tomato vegetative shoots including
meristems and small expanding leaves."
BASE COUNT      192 a      127 c      150 g      168 t
ORIGIN

Query Match      78.7%; Score 613.8; DB 9; Length 637;
Best Local Similarity 99.4%; Pred. No. 6.1e-108;
Matches 627; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY      2 aagaatcctagagagaagaagaatccttagagagaagatgtcgagcaagaacac 61
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      7 AGGAATCCTAGAGAGAGAAAGGAATCCTAGAGAGAGATGCGAGCAAGACACC 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      62 atttgaatcaagaacatgtgtgtgtcctcaaaaacttcccaagaactggaacca 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      67 ATTTGAGTCAAGGCAATGCTGTGCTCAAAAACCTTCCACAGCAAGCTGMAACA 126
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      122 tccgtaagaatgttacatcgltatcaaaagccgtccctgaaggttgtaggtcca 181
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      127 TCCGTAAAGATGTGTACATCGTTATCAAAAGGCCGCTCCGCAAGTTGTTGAGCTCCA 186
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      182 cttcaaaaactggaaaaacagcgacatgctaagtacattgttggaattgaatttca 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      187 CTTCAAAAACGTGGAAAGACAGGACATGCTAAATGTCATTTGTGGCAATTTTCA 246
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      242 atggaagaagaactggaagatatcgltccgtccctcccaaatgtgtagtgcacatgta 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      247 AAGGAAGAAGAACTGGAAGATATCGTTCGTCCTCCACAAATGTGATGTGCGACATGTA 306
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      302 accgtacacgactatcagctgattgatctctgaagaatgtttgtctacttctactg 361
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      307 ACCGTACCGACTATCATCGTATGTATCTGTGAAGATGTTTGTCTCACTTTCTACTG 366
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      362 aagatggaacacccaagaatgacctcaagcttcccaacgataatctgtctgaacag 421
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      367 AAAGTGAAGAACCCAAAGATGACCTCAGCGTTCCACCGATGAANAATGCTGTGAACAG 426
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      422 ttaaaagtgtgttccagaagaagaatcttgtgtgtgtctgtatgtctgtcgtatg 481
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      427 TTAAGATGTGGTTCAGAGAAAGGATCTTGTGTGTCTGTATGTCTCGATGGGCG 486
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      482 aaggaacaattaacgcttgaagtgtgtgttaccagaatagtatgtcatgtgcagc- 540
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      487 AAGACAGATTTAACCGCGTTAAGATGTGTGACCAAAATTAAGTTATGTATGTATGCA 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      541 -ataatcactgcacaagcttaagaacattatcattcctaattgtctgaacttgcatac 599
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      547 TATATCACTGCCAAGCTTTAAGACATTATCAATATCTTAATGTGTGTTGATATACAC 606
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      600 tagattataaactgtgtattgtcacgtgtc 630
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      607 TAGATTATAAAGCTGTATTGTGACACTGTTC 637
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
LOCUS      AM622132      654 bp      mRNA      linear      EST 18-MAY-2001
DEFINITION EST312930 tomato root during/after fruit set, Cornell University
LYCopersicon esculentum cDNA clone cLEX14G22 5', mRNA sequence.
ACCESSION  AM622132
VERSION     AM622132.1 GI:7333779
KEYWORDS   EST.
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.

```

```

REFERENCE      1 (bases 1 to 654)
AUTHORS      van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Kochian,L.,
            Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M.,
            Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,D.J. and Tanksley
            S.D.
TITLE        Generation of ESTs from tomato root, during and after fruit set
JOURNAL      Unpublished (1999)
COMMENT      Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES
    source      Location/Qualifiers
                1..654
                /organism="Lycopersicon esculentum"
                /cultivar="74A96"
                /db_xref="taxon:4081"
                /clone="cLEX14G22"
                /clone.lib="tomato root during/after fruit set, Cornell
            University"
                /issue_type="root"
                /dev_stage="plants during and after fruit-set"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI, Site_2:
            XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
            (USDA-ARS, Ithaca, NY 14850)."
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QY 599 ctgattataaactgtgtatttgcacgttgc 630  
 |||||||  
 Db 623 CTGATTATTAACACTGTGTTATTGCACTGTC 654

RESULT 12  
 BI203884  
 LOCUS ESTS212924 cTOS Lycopersicon esculentum cDNA clone cTOS3122 5' end,  
 DEFINITION mRNA sequence.  
 BI203884  
 VERSION BI203884.1 GI:14681608  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 624)  
 van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,  
 Ronning, C. and Tanksley, S.  
 Generation of ESTs from Tomato Suspension Cultures  
 Unpublished (2001)  
 CONTACT: CUGI  
 CLEMSON UNIVERSITY GENOMICS INSTITUTE  
 CLEMSON UNIVERSITY  
 100 JORDAN HALL, CLEMSON, SC 29634, USA  
 EMAIL: <http://www.genome.clemson.edu/orders/index.html>.  
 Location/Qualifiers  
 1..624  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496, E6203"  
 /db\_xref="taxon:4081"  
 /clone="cTOS3122"  
 /clone\_lib="cTOS"  
 /tissue\_type="suspension cultures"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Suspension cultures of L.esculentum E6203 were grown  
 in Murashige and Skoog based medium, supplemented with 15%  
 coconut milk (filter sterilized and added after  
 autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).  
 Fresh medium was added every 7 days, and cultures were  
 grown at 25 C, with 12hrs of light and continuous  
 shaking."

BASE COUNT 189 a 120 c 138 g 177 t  
 ORIGIN

Query Match 77.7%; Score 605.8; DB 10; Length 624;  
 Best Local Similarity 99.4%; Pred. No. 2,1e-106;  
 Matches 619; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 100 ttccacacgaagctggaacatccgtaagaatggttaccgtttatacaagccgtccc 159  
 |||||||  
 Db 2 TTTCACACAGAGCTGGAACCATCCGTAAGATGGTTACATGCTTATTAAGGCCGCTCCC 61

QY 160 tgcgaagtgttgagggtctccacttcaaaaactggaacacgacgacgtctaaatgtcac 219  
 |||||||  
 Db 62 TGCAGAGTGTGAGGTCTCCACTTCAAAAACCTGGAAGACGACATGCTAAATGTCCAC 121

QY 220 ttgttgacatgacatcttcaatggaagaacatggaagataatcgttcgctccacac 279  
 |||||||  
 Db 122 TTTGTGGCAATTGACATTTTCAATGGAAGAACTGGAAGATATGCTTCGCTCCACAC 181

QY 280 aattgtagtgcacatgttaaccgttaacgacatacgcgtatgatatctctgaagat 339  
 |||||||  
 Db 182 AATTGAGATGTGACACATTTTAACCGTACCGACTATCAGCTGATTAATCTCTGAAGAT 241

QY 340 ggtttgtctcacttcttacttgaagtgaaacacacgaagtgacctgacctccacac 399  
 |||||||

Db 242 GGTTTGTCTCAGCTTCTTACTGAAAGTGAACACCAAGATGACCTCAGGCTTCCACC 301

QY 400 gatgaaaaatctgtctgaagcaaggttaagaatggttccaggaaggaagatcttgggtg 439  
 |||||||  
 Db 302 GATGAAAATCTGTGAAGCAGGTTAAAGATGGTTCCAGGAAGGAAGGATCTTGTGTG 361

QY 460 tctgtatgtctgcgtgagggcgaagagacagatlaacgcccttaagagatgttggagacaag 519  
 |||||||  
 Db 362 TCTGTTATGTCTGCGATGGGGGGAAGACAGATTAAACCCGTTAAAGATGTTGGTACCAAG 421

QY 520 aattgatatgtcatggaagc--ataatcactgcgaagccttlaagacattatcatatcc 577  
 |||||||  
 Db 422 AATTAGTTATGTCAATGCGACAGCATATTAATCACTGCCAAGCCTTTAAAGCATTAATATTC 481

QY 578 taatgtgtactttgatatactactagattataaactgtgtatttgcacgttcaaaaaca 637  
 |||||||  
 Db 482 TAAAGTGCTACTTTGATATCACTAGAAATTAATAACTGTATTATTTGCACTGTCCAAAACAA 541

QY 638 aagaagaacacgtctgtatgctagaagaagatgtgctttgagcttttgaacagaca 697  
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 Db 542 AAGAAAGAAAACCTGCTGTATGGCTAGAGAAAGATTAATGGCTTTGACAGCACA 601

QY 698 gttagaatatgtgaattctac 720  
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 Db 602 GTTGACTATGTGAATAATTTCTAC 624

RESULT 13  
 BI205158  
 LOCUS ESTS23198 cTOS Lycopersicon esculentum cDNA clone cTOS7M5 5' end,  
 DEFINITION mRNA sequence.  
 BI205158  
 VERSION BI205158.1 GI:14682882  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 622)  
 van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,  
 Ronning, C. and Tanksley, S.  
 Generation of ESTs from Tomato Suspension Cultures  
 Unpublished (2001)  
 CONTACT: CUGI  
 CLEMSON UNIVERSITY GENOMICS INSTITUTE  
 CLEMSON UNIVERSITY  
 100 JORDAN HALL, CLEMSON, SC 29634, USA  
 EMAIL: <http://www.genome.clemson.edu/orders/index.html>.  
 Location/Qualifiers  
 1..622  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496, E6203"  
 /db\_xref="taxon:4081"  
 /clone="cTOS7M5"  
 /clone\_lib="cTOS"  
 /tissue\_type="suspension cultures"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Suspension cultures of L.esculentum E6203 were grown  
 in Murashige and Skoog based medium, supplemented with 15%  
 coconut milk (filter sterilized and added after  
 autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).  
 Fresh medium was added every 7 days, and cultures were  
 grown at 25 C, with 12hrs of light and continuous  
 shaking."

BASE COUNT 190 a 123 c 146 g 163 t  
 ORIGIN

Query Match 77.3%; Score 603.2; DB 10; Length 622;

Best Local Similarity 99.2%; Pred. No. 6.5e-106;  
Matches 617; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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QY 4 gatcttagaagaagaagaatccttagaagaagaacatgctcggaagaagaacacat 63
   |||||||
Db 1 GAATCCTTAGAGAGAAAGGAGATCTTAGAGAGAAACATGTGGAGAGAACACCAT 60
QY 64 ttgtgataaaggcagatgctgctcctcaaaacttccacagcaagctggaacatc 123
   |||||||
Db 61 TTTGAGTCAAGAGGAGATGCTGGTCCCTCAAAACTTCCACAGCAAGCTGGAACCATC 120
QY 124 cgttaagaatggttacatcgtttacaagaagccgtccctgcaaggtgtgtgaagttccact 183
   |||||||
Db 121 CCTAAGATGTTGATCATGTATCAAAAGCCGCTCCCTCCAGAGTGTGTGAGCTCCACT 180
QY 184 tcaaaaactggaaaacaggaacatgcttaaatgctacttctgggaatggaactttcaat 243
   |||||||
Db 181 TCAAAACCTGGAAACAGCAAGCATCTAAATGTCACTTGTGGCAATTGACATTTTCAT 240
QY 244 ggaagaacactggaagatatacgttcgctccctccacaacttgtagtgcacatgtaac 303
   |||||||
Db 241 GGAAGAAACCTGGAAGATATGTTCCGCTCCCTCCACATTTGTGATGTGCCACATGTTAAC 300
QY 304 cgtaccgactatcagctgatactctctgaaagatgttttctcaacttctactgaa 363
   |||||||
Db 301 CTTACCGACTATCAGCTGATGTATCTGTGAAGTGTGTGTCTCACTTCTTACTGAA 360
QY 364 agtggaaacacaaagatgactcagcttcgctccacagatgaatactgcaagcaggt 423
   |||||||
Db 361 AGTGGAAACACCAAGATGACTCTCAGGCTTCCACCGATGAAATCTGCTAAGCAGGTT 420
QY 424 aaagatggtgtccaggaagaagaatctgtgtgtctgttactgtcgtcgaatgagcga 483
   |||||||
Db 421 AAAGATGAGTTCAGAGAGAAAGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 484 gggcagatgaagcggtaagaatgtgtgtccaaagaattgttatgtcagagcagc--a 541
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Db 481 GAGCAGATTAAAGCGGTAAAGATGTGTGTACCAAGATTTGATTTGTCATGAGCACTA 540
QY 542 taatactgccaagaacttaagaacatatacatalactcaatgtgtgtactgtatataccta 601
   |||||||
Db 541 TAAATCACTGCCAAAGCTTTAAGACATTAATCAATTCCTAATGTGACTTTGATATCACTA 600
QY 602 gattataactgtgttatttgc 623
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Db 601 GAATATAAACTGTGTATTTGC 622

```

## RESULT 14

BE451409 617 bp mRNA linear EST 18-MAY-2001  
LOCUS EST402297 tomato root, plants pre-anthesis, Cornell University  
DEFINITION Lycopersicon esculentum cDNA clone CLEY18J1, mRNA sequence.  
ACCESSION BE451409  
VERSION BE451409.1 GI:9456912  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 617)  
van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,  
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,  
, Frazer,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.  
Generation of ESTs from tomato root tissue  
unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>

TITLE  
JOURNAL  
COMMENT

FEATURES 5 prime sequence.  
Location/Qualifiers  
1..617  
/organism="Lycopersicon esculentum"  
/cultivar="NA496"  
/db\_xref="taxon:4081"  
/clone="CLEY18J1"  
/clone\_1ib="tomato root, plants pre-anthesis, Cornell  
University"  
/tissue\_type="root"  
/dev\_stage="plants in pre-anthesis stage"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI, Site\_2:  
XhoI; supplier: Tanksley; tissue supplied by Dave Garvin  
(USDA-ARS, Ithaca, NY 14850)."  
BASE COUNT 192 a 126 c 143 g 156 t  
ORIGIN

Query Match 75.4%; Score 588.4; DB 10; Length 617;  
Best Local Similarity 99.5%; Pred. No. 4.5e-103;  
Matches 601; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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QY 1 aaagaatcctaagagagaagaagaaatccttagaagaagaacatgctcggaagaagaac 60
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Db 14 AAAAGATCCTAGAGAGAGAAAGGAAATCCTAGAGAGAAAGATGTGGAGCAAGAACAC 73
QY 61 catttgatcaagaagcagatgctgtgtgtcctcaaaacttccacagaagaactggaacc 120
   |||||||
Db 74 CATTTTGAGTCAAGAGAGATGCTGTGTGCTCAAAACTTCCACAGCAAGCTGGAAC 133
QY 121 atccgtaagaatggttacatcgtttacaagaagcgcgtccctgcaaggtgtgtgaagttcc 180
   |||||||
Db 134 ATCCGTAAAGATGTTATCATCTATCAAAAGGCGCTCCGCAAGGTTGTGAGTCTCC 193
QY 181 acttcaaaaacttgaaaacacagacatgctaaatgctacttgtgtgcaattgaacatttc 240
   |||||||
Db 194 ACTTCAAAAACCTGAAAGCAGCAATGCTAAATGTGACTTTGTGCAATGACATTTTC 253
QY 241 aatggaagaagaactggaagatatacgttcgctccctccacaatgtgatagtgtgcacatgt 300
   |||||||
Db 254 AATGGAAGAAAGCTGGAAGATATGTTCCGCTCCACAAATGTGTGTGTGTGTGTGTGTGT 313
QY 301 aaccgtacgactatacagctgattgatatctctgaaagatgtgtgtgtgtgtgtgtgtgtgt 360
   |||||||
Db 314 AACCGTACCGACTATCAGCTGATTTGATCTTGAAGATGTTTGTCTCACTTCTTACT 373
QY 361 gaaagtgaacaacaaagatgaccccaagctcccaacgaatgaatgaatgctgtgaagcag 420
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Db 374 GAAGTGGAAACACCAAGATGACCTCAGGCTTCCACCGATGAAATGCTGGAAGCAG 433
QY 421 gttaaagatggttccagagaagaagaatcctgtgtgtgttactgtctcgtcgaatgagc 480
   |||||||
Db 434 GTTAAAGATGAGTTCAGAGAGAAAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 493
QY 481 gaagaagcagatlaagcgcgtlaagatgtgtgtaccaaagaatagttatgtatcattgacgc 540
   |||||||
Db 494 GAAGAGCAGATTAAAGCCTGTTAAGATGTGTGTAACCAAGATTAAGTATGATGCTAGCAGC 553
QY 541 --taatacactgccaagaacttaagaacatatacatalactcaatgtgtgtgtgtgtgtgtgt 598
   |||||||
Db 554 ATATATCACTGCCAAAGCTTTAAGACATTAATCAATTAATGTGTGTGTGTGTGTGTGTGT 613
QY 599 ctga 602
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Db 614 CTAG 617

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## RESULT 15

BS590355 645 bp mRNA linear EST 12-APR-2001  
LOCUS BS590355  
DEFINITION EST498197 P. infestans-challenged leaf Solanum tuberosum cDNA clone  
BPL14H16 5' sequence, mRNA sequence.  
ACCESSION BS590355



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